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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/083,620A

DATE: 06/06/2002
 TIME: 15:05:43

Input Set : A:\38275.txt
 Output Set: N:\CRF3\06062002\J083620A.raw

p.6

3 <110> APPLICANT: Loughney, Kate
 5 <120> TITLE OF INVENTION: Phosphodiesterase 10
 7 <130> FILE REFERENCE: 27866/38275
 9 <140> CURRENT APPLICATION NUMBER: 10/083,620A
 10 <141> CURRENT FILING DATE: 2002-05-30

ENTERED

12 <150> PRIOR APPLICATION NUMBER: 09/256,000
 13 <151> PRIOR FILING DATE: 1999-02-23
 15 <150> PRIOR APPLICATION NUMBER: 60/075,508
 16 <151> PRIOR FILING DATE: 1998-02-23
 18 <160> NUMBER OF SEQ ID NOS: 26
 20 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1548
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (26)..(1423)
 31 <400> SEQUENCE: 1

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33                               Met Asp Ala Phe Arg Ser Thr Pro Tyr
34                               1           5
36 aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta 100
37 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
38 10           15           20           25
40 atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
41 Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
42           30           35           40
44 aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 196
45 Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
46           45           50           55
48 gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
49 Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
50           60           65           70
52 tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
53 Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
54           75           80           85
56 agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
57 Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
58 90           95           100           105
60 aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 388
61 Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
62           110           115           120

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64 tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg 436
65 Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
66 125 130 135
68 ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac 484
69 Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
70 140 145 150
72 gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg 532
73 Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg
74 155 160 165
76 agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac 580
77 Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His
78 170 175 180 185
80 aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc 628
81 Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val
82 190 195 200
84 tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc 676
85 Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile
86 205 210 215
88 cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac 724
89 Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn
90 220 225 230
92 aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat 772
93 Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn
94 235 240 245
96 gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc 820
97 Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile
98 250 255 260 265
100 ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg 868
101 Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly
102 270 275 280
104 ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac 916
105 Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp
106 285 290 295
108 atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag 964
109 Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu
110 300 305 310
112 aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att 1012
113 Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile
114 315 320 325
116 ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc 1060
117 Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val
118 330 335 340 345
120 gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc 1108
121 Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
122 350 355 360
124 gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga 1156
125 Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
126 365 370 375
128 gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc 1204

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Input Set : A:\38275.txt

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129 Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
130      380      385      390
132 ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag 1252
133 Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
134      395      400      405
136 gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1300
137 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
138 410      415      420      425
140 ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1348
141 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
142      430      435      440
144 agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat 1396
145 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
146      445      450      455
148 gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggagcgtg 1443
149 Val Lys Asn Ser Glu Gly Asp Cys Ala
150      460      465
152 gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503
154 ctgggcacct ggcaccacaa gaccatgttt tctaagaacc atttt 1548
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 466
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 2
163 Met Asp Ala Phe Arg Ser Thr Pro Tyr Lys Val Arg Pro Val Ala Ile
164 1 5 10 15
166 Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln
167 20 25 30
169 Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
170 35 40 45
172 Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
173 50 55 60
175 Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
176 65 70 75 80
178 Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
179 85 90 95
181 Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
182 100 105 110
184 Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
185 115 120 125
187 Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
188 130 135 140
190 Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
191 145 150 155 160
193 Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
194 165 170 175
196 Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
197 180 185 190
199 Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu

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Input Set : A:\38275.txt
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200          195          200          205
202 Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
203          210          215          220
205 His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
206 225          230          235          240
208 Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
209          245          250          255
211 His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
212          260          265          270
214 Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
215          275          280          285
217 Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
218          290          295          300
220 Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
221 305          310          315          320
223 Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
224          325          330          335
226 Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
227          340          345          350
229 Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
230          355          360          365
232 Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
233          370          375          380
235 Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
236 385          390          395          400
238 Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
239          405          410          415
241 Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
242          420          425          430
244 Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
245          435          440          445
247 Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
248          450          455          460
250 Cys Ala
251 465
254 <210> SEQ ID NO: 3
255 <211> LENGTH: 225
256 <212> TYPE: DNA
257 <213> ORGANISM: Homo sapiens
259 <220> FEATURE:
W--> 260 <221> NAME/KEY: misc feature
261 <222> LOCATION: 130
262 <223> OTHER INFORMATION: N = A, T, G, or C
264 <220> FEATURE:
W--> 265 <221> NAME/KEY: misc feature
266 <222> LOCATION: 186
267 <223> OTHER INFORMATION: N = A, T, G, or C
269 <220> FEATURE:
W--> 270 <221> NAME/KEY: misc feature

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 PATENT APPLICATION: US/10/083,620A

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 TIME: 15:05:43

Input Set : A:\38275.txt
 Output Set: N:\CRF3\06062002\J083620A.raw

271 <222> LOCATION: 205
 272 <223> OTHER INFORMATION: N = A, T, G, or C
 274 <400> SEQUENCE: 3
 275 agcgaccgtg agaagtcaga aggccttcct gtggaaccgt tcatggaccg agacaaagtg 60
 277 accaaggcca cagcccagat tgggttcacg aagtttgccc tgatcccaat gtttgaaaca 120
 W--> 279 gtgaccaagn tcttccccat gggtgaggag atcatgctgc agccacttg ggaatccccga 180
 W--> 281 gatcgntacg aggagctgaa gcggntagat gacgccatga aagag 225
 284 <210> SEQ ID NO: 4
 285 <211> LENGTH: 158
 286 <212> TYPE: DNA
 287 <213> ORGANISM: Homo sapiens
 289 <220> FEATURE:
 W--> 290 <221> NAME/KEY: misc feature
 291 <222> LOCATION: 12
 292 <223> OTHER INFORMATION: N = A, T, G, or C
 295 <220> FEATURE:
 W--> 296 <221> NAME/KEY: misc feature
 297 <222> LOCATION: 37
 298 <223> OTHER INFORMATION: N = A, T, G, or C
 300 <220> FEATURE:
 W--> 301 <221> NAME/KEY: misc feature
 302 <222> LOCATION: 62
 303 <223> OTHER INFORMATION: N = A, T, G, or C
 305 <220> FEATURE:
 W--> 306 <221> NAME/KEY: misc feature
 307 <222> LOCATION: 110
 308 <223> OTHER INFORMATION: N = A, T, G, or C
 310 <400> SEQUENCE: 4
 W--> 311 gtaccagatc antgcccgca cagagctggc ggtccgntac aatgacatct caccgttgga 60
 W--> 313 gnaaccacca ctgcgccgtg gccttcacga tcctcgccga gcctgagtgn aacatcttct 120
 315 ccaacatccc acctgatggg ttcaagcaga tccgacag 158
 318 <210> SEQ ID NO: 5
 319 <211> LENGTH: 98
 320 <212> TYPE: DNA
 321 <213> ORGANISM: Homo sapiens
 323 <220> FEATURE:
 W--> 324 <221> NAME/KEY: misc feature
 325 <222> LOCATION: 14
 326 <223> OTHER INFORMATION: N = A, T, G, or C
 328 <220> FEATURE:
 W--> 329 <221> NAME/KEY: misc feature
 330 <222> LOCATION: 22
 331 <223> OTHER INFORMATION: N = A, T, G, or C
 333 <220> FEATURE:
 W--> 334 <221> NAME/KEY: misc feature
 335 <222> LOCATION: 50
 336 <223> OTHER INFORMATION: N = A, T, G, or C
 338 <400> SEQUENCE: 5
 W--> 339 gagaacacca ctgngccgtg gncttcacga tcctcgccga gcctgagtgn aacatcttct 60

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/083,620A

DATE: 06/06/2002
TIME: 15:05:44

Input Set : A:\38275.txt
Output Set: N:\CRF3\06062002\J083620A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 130,186,205
Seq#:4; N Pos. 12,37,62,110
Seq#:5; N Pos. 14,22,50
Seq#:6; N Pos. 1,267,352,400,411
Seq#:7; N Pos. 1,82,92,130,347,390,396
Seq#:8; N Pos. 63,98,107,188,203,206,238,252,297,370,389,427
Seq#:11; N Pos. 155,393,442